IN THE CLAIMS

Please amend claims 2 and 4 as follows.

1. (Canceled)

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2. (Currently Amended) A substantially purified polynucleotide, or the complete complement thereof, comprising a polynucleotide sequence selected from:

(a) a polynucleotide sequence ~~selected from the group consisting~~ of SEQ ID NOs:~~1-5~~ 4;

(b) a polynucleotide sequence which encodes the polypeptide sequence of SEQ ID NO: 6; and

(c) ~~a polynucleotide sequence which is completely complementary to the polynucleotide sequence of (a) or (b); and~~

~~(d)~~ a naturally-occurring variant of the polynucleotide of (a)~~, (b), or (c)~~, having at least 95% identity to the polynucleotide sequence of (a)~~, (b), or (c)~~.

3. (Canceled)

4. (Currently Amended) A substantially purified polypeptide, comprising a polypeptide sequence selected from:

(a) the polypeptide sequence of SEQ ID NO: 6; and

(b) an immunogenic fragment of the polypeptide sequence of (a) comprising at least 6 sequential amino acids of the polypeptide sequence of (a)~~; and~~

~~(c) a variant of the polypeptide sequence of SEQ ID NO:6 having at least 95% identity to the polypeptide sequence of SEQ ID NO:6~~.

5. (Original) An expression vector comprising the polynucleotide of claim 2.

6. (Original) A host cell comprising the expression vector of claim 5.

7. (Previously Amended) A composition comprising the polynucleotide of claim 2 in conjunction with a suitable pharmaceutical carrier.

8. (Previously Amended) A composition comprising the polypeptide of claim 4 in conjunction with a suitable pharmaceutical carrier.

9. (Original) An antibody which specifically binds to the polypeptide of claim 4.

10. (Original) A method for diagnosing a disease or condition associated with the altered expression of a gene that is coexpressed with one or more neurotransmitter-processing-

specific genes, wherein each neurotransmitter-processing-specific gene is selected from the group consisting of L-tyrosine hydroxylase (TH), aromatic amino acid decarboxylase (AADC), dopamine β-hydroxylase (DBH), nicotinic acetylcholine receptor α3 subunit precursor (nAchR-α3), secretogranin I and II, Rab3a, human cocaine and amphetamine regulated transcript (hCART), vesicular monoamine transporter 1 (hVMAT1), and ARIX homeodomain protein, the method comprising the steps of:

(a) providing a sample comprising one of more of said coexpressed genes;

(b) hybridizing the polynucleotide of claim 2 to said coexpressed genes under conditions effective to form one or more hybridization complexes; and

(c) detecting the hybridization complexes, wherein the presence of the hybridization complexes correlates with the presence of the disease or condition.

11. (Canceled)

12. (Previously Added) A composition comprising a plurality of polynucleotides wherein the polynucleotides consist of the nucleic acid sequences of SEQ ID NOs:1-5 or the complements thereof.

13 (Previously Added) The composition of claim 12 and a labeling moiety.

14. (Previously Added) A method for using a polynucleotide to detect gene expression in a sample, the method comprising:

(a) hybridizing the composition of claim 13 to a sample thereby forming at least one hybridization complex;

(b) detecting complex formation, wherein complex formation indicates gene expression in the sample.

15. (Previously Added) The method of claim 14 wherein gene expression is compared to standards and is diagnostic of Parkinson's disease, schizophrenia, or epilepsy.